

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wassenegger, Michael
Riedel, Leonhard
Schiebel, Winfried
Sanger, Heinz
- (ii) TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN
RNA-DIRECTED RNA POLYMERASE (RdRP)
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: FISH & NEAVE
 - (B) STREET: 1251 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10020
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/811,583
 - (B) FILING DATE: 05-MAR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Haley, James F.
 - (B) REGISTRATION NUMBER: 27,794
 - (C) REFERENCE/DOCKET NUMBER: MPG-1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 212-596-9000
 - (B) TELEFAX: 212-596-9090

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3731 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tomato
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 194..3535

Express Mail Label
EI187447517US

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAAATATTCT TTACTTACTT CACCAGGGAT TGACTCATCA CTCCCCTCAA GTCTTTGTGT	60
TTTGTGATAA TAAATTTGGT TGTGCTTCAG TTTCAGTCAC TACTGCTGGG TAGTTTTTAT	120
TTTGCATAAC TTCAGGGGGT ATTCCAGTTG GTGTTAGCAT TTGAAAGTCG AACTGCACTT	180
GGAATTTGGC TAC ATG GGA AAG ACA ATT CAG GTT TTC GGA TTC CCT TAT	229
Met Gly Lys Thr Ile Gln Val Phe Gly Phe Pro Tyr	
1 5 10	
CTT CTC TCT GCG GAA GTG GTT AAG TCA TTC TTA GAG AAA TAT ACA GGA	277
Leu Leu Ser Ala Glu Val Val Lys Ser Phe Leu Glu Lys Tyr Thr Gly	
15 20 25	
TAT GGA ACT GTA TGT GCA TTG GAG GTT AAA CAG TCC AAA GGA GGA TCT	325
Tyr Gly Thr Val Cys Ala Leu Glu Val Lys Gln Ser Lys Gly Gly Ser	
30 35 40	
AGA GCA TTT GCC AAA GTT CAA TTT GCC GAC AAC ATA AGT GCT GAC AAA	373
Arg Ala Phe Ala Lys Val Gln Phe Ala Asp Asn Ile Ser Ala Asp Lys	
45 50 55 60	
ATC ATC ACT TTG GCT AAT AAC AGG CTG TAT TTT GGC TCT TCT TAT TTG	421
Ile Ile Thr Leu Ala Asn Asn Arg Leu Tyr Phe Gly Ser Ser Tyr Leu	
65 70 75	
AAG GCT TGG GAA ATG AAA ACT GAT ATT GTC CAA CTG CGG GCA TAT GTG	469
Lys Ala Trp Glu Met Lys Thr Asp Ile Val Gln Leu Arg Ala Tyr Val	
80 85 90	
GAT CAG ATG GAT GGC ATA ACT TTG AAT TTC GGA TGT CAG ATA TCA GAT	517
Asp Gln Met Asp Gly Ile Thr Leu Asn Phe Gly Cys Gln Ile Ser Asp	
95 100 105	
GAC AAG TTT GCA GTG TTG GGA AGT ACA GAA GTT TCA ATT CAA TTT GGC	565
Asp Lys Phe Ala Val Leu Gly Ser Thr Glu Val Ser Ile Gln Phe Gly	
110 115 120	
ATT GGA TTG AAG AAA TTT TTT TTC TTT TTA TCT AGT GGT TCA GCT GAC	613
Ile Gly Leu Lys Lys Phe Phe Phe Phe Leu Ser Ser Gly Ser Ala Asp	
125 130 135 140	
TAT AAA CTT CAG CTT TCA TAT GAA AAT ATA TGG CAG GTT GTG CTC CAT	661
Tyr Lys Leu Gln Leu Ser Tyr Glu Asn Ile Trp Gln Val Val Leu His	
145 150 155	
CGT CCA TAT GGT CAA AAT GCT CAG TTT CTC CTC ATA CAG TTA TTT GGT	709
Arg Pro Tyr Gly Gln Asn Ala Gln Phe Leu Leu Ile Gln Leu Phe Gly	
160 165 170	
GCT CCT CGG ATC TAT AAG AGA CTT GAA AAC TCC TGT TAT AGC TTC TTT	757
Ala Pro Arg Ile Tyr Lys Arg Leu Glu Asn Ser Cys Tyr Ser Phe Phe	
175 180 185	
AAG GAA ACT CCT GAT GAT CAG TGG GTG AGG ACA ACA GAT TTC CCT CCA	805
Lys Glu Thr Pro Asp Asp Gln Trp Val Arg Thr Thr Asp Phe Pro Pro	
190 195 200	

TCT	TGG	ATA	GGG	CTA	TCT	TCT	AGC	TTA	TGT	TTG	CAG	TTC	CGT	AGG	GGT	853
Ser	Trp	Ile	Gly	Leu	Ser	Ser	Ser	Leu	Cys	Leu	Gln	Phe	Arg	Arg	Gly	
205					210					215					220	
GTT	CGT	CTT	CCA	AAT	TTC	GAG	GAA	AGT	TTT	TTC	CAC	TAT	GCA	GAA	CGT	901
Val	Arg	Leu	Pro	Asn	Phe	Glu	Glu	Ser	Phe	Phe	His	Tyr	Ala	Glu	Arg	
				225					230					235		
GAA	AAC	AAT	ATT	ACT	TTA	CAG	ACT	GGT	TTC	ACC	TTT	TTC	GTC	TCT	CAA	949
Glu	Asn	Asn	Ile	Thr	Leu	Gln	Thr	Gly	Phe	Thr	Phe	Phe	Val	Ser	Gln	
			240					245					250			
AAA	TCG	GCT	CTG	GTT	CCC	AAT	GTC	CAG	CCT	CCG	GAA	GGA	ATT	TCA	ATT	997
Lys	Ser	Ala	Leu	Val	Pro	Asn	Val	Gln	Pro	Pro	Glu	Gly	Ile	Ser	Ile	
		255					260					265				
CCC	TAC	AAG	ATT	TTG	TTC	AAA	ATT	AGT	TCT	TTG	GTA	CAG	CAT	GGA	TGC	1045
Pro	Tyr	Lys	Ile	Leu	Phe	Lys	Ile	Ser	Ser	Leu	Val	Gln	His	Gly	Cys	
	270					275					280					
ATA	CCT	GGG	CCA	GCA	TTA	AAT	GTC	TAC	TTT	TTC	CGA	TTA	GTT	GAT	CCT	1093
Ile	Pro	Gly	Pro	Ala	Leu	Asn	Val	Tyr	Phe	Phe	Arg	Leu	Val	Asp	Pro	
285					290					295					300	
CGA	AGG	AGA	AAT	GTG	GCA	TGC	ATT	GAG	CAT	GCC	TTA	GAG	AAA	CTG	TAC	1141
Arg	Arg	Arg	Asn	Val	Ala	Cys	Ile	Glu	His	Ala	Leu	Glu	Lys	Leu	Tyr	
			305					310						315		
TAT	ATA	AAG	GAG	TGC	TGT	TAT	GAT	CCC	GTG	AGG	TGG	CTC	ACT	GAG	CAG	1189
Tyr	Ile	Lys	Glu	Cys	Cys	Tyr	Asp	Pro	Val	Arg	Trp	Leu	Thr	Glu	Gln	
			320					325					330			
TAT	GAT	GGG	TAT	CTC	AAG	GGT	AGA	CAA	CCT	CCA	AAA	TCT	CCG	TCC	ATC	1237
Tyr	Asp	Gly	Tyr	Leu	Lys	Gly	Arg	Gln	Pro	Pro	Lys	Ser	Pro	Ser	Ile	
		335					340					345				
ACT	TTA	GAT	GAT	GGG	TTG	GTG	TAT	GTA	AGA	AGG	GTC	CTA	GTA	ACA	CCA	1285
Thr	Leu	Asp	Asp	Gly	Leu	Val	Tyr	Val	Arg	Arg	Val	Leu	Val	Thr	Pro	
	350					355					360					
TGC	AAA	GTT	TAT	TTT	TGT	GGT	CCA	GAG	GTT	AAT	GTT	TCC	AAT	CGG	GTT	1333
Cys	Lys	Val	Tyr	Phe	Cys	Gly	Pro	Glu	Val	Asn	Val	Ser	Asn	Arg	Val	
365					370					375					380	
CTC	CGC	AAT	TAT	TCT	GAA	GAC	ATA	GAT	AAC	TTT	CTT	CGT	GTT	TCT	TTT	1381
Leu	Arg	Asn	Tyr	Ser	Glu	Asp	Ile	Asp	Asn	Phe	Leu	Arg	Val	Ser	Phe	
				385					390					395		
GTT	GAT	GAG	GAG	TGG	GAG	AAA	CTG	TAT	TCT	ACA	GAC	TTA	TTA	CCA	AAA	1429
Val	Asp	Glu	Glu	Trp	Glu	Lys	Leu	Tyr	Ser	Thr	Asp	Leu	Leu	Pro	Lys	
			400					405					410			
GCA	AGT	ACT	GGA	AGT	GGT	GTC	AGG	ACA	AAC	ATC	TAT	GAG	AGG	ATC	TTA	1477
Ala	Ser	Thr	Gly	Ser	Gly	Val	Arg	Thr	Asn	Ile	Tyr	Glu	Arg	Ile	Leu	
		415				420						425				
TCA	ACT	CTG	CGG	AAA	GGC	TTT	GTA	ATT	GGT	GAT	AAA	AAA	TTT	GAA	TTT	1525
Ser	Thr	Leu	Arg	Lys	Gly	Phe	Val	Ile	Gly	Asp	Lys	Lys	Phe	Glu	Phe	
	430					435					440					

CTT Leu 445	GCA Ala	TTT Phe	TCA Ser	TCG Ser	AGC Ser 450	CAG Gln	TTG Leu	CGG Arg	GAT Asp	AAT Asn 455	TCA Ser	GTG Val	TGG Trp	ATG Met	TTT Phe 460	1573
GCA Ala	TCA Ser	AGA Arg	CCT Pro	GGC Gly 465	CTT Leu	ACT Thr	GCA Ala	AAT Asn 470	GAT Asp	ATA Ile	AGA Arg	GCT Ala	TGG Trp	ATG Met 475	GGT Gly	1621
GAT Asp	TTT Phe	TCG Ser	CAG Gln 480	ATC Ile	AAG Lys	AAT Asn	GTC Val	GCA Ala 485	AAA Lys	TAT Tyr	GCT Ala	GCC Ala	AGA Arg 490	CTT Leu	GGT Gly	1669
CAA Gln	TCT Ser	TTT Phe 495	GGT Gly	TCC Ser	TCC Ser	AGA Arg	GAG Glu 500	ACT Thr	TTG Leu	AGT Ser	GTT Val	CTT Leu 505	AGG Arg	CAT His	GAG Glu	1717
ATT Ile 510	GAA Glu	GTT Val	ATT Ile	CCC Pro	GAT Asp	GTA Val 515	AAG Lys	GTT Val	CAT His	GGA Gly 520	ACC Thr	AGC Ser	TAT Tyr	GTC Val	TTT Phe	1765
TCT Ser 525	GAT Asp	GGA Gly	ATT Ile	GGT Gly 530	AAA Lys	ATA Ile	TCT Ser	GGT Gly	GAC Asp	TTT Phe 535	GCT Ala	CAT His	AGA Arg	GTT Val	GCC Ala 540	1813
TCA Ser	AAA Lys	TGT Cys	GGC Gly	CTT Leu 545	CAA Gln	TAT Tyr	ACC Thr	CCA Pro	TCT Ser 550	GCT Ala	TTC Phe	CAG Gln	ATT Ile	CGT Arg 555	TAT Tyr	1861
GGT Gly	GGA Gly	TAT Tyr	AAA Lys 560	GGT Gly	GTT Val	GTG Val	GGT Gly 565	GTT Val	GAT Asp	CCG Pro	GAT Asp	TCA Ser	TCA Ser 570	ATG Met	AAG Lys	1909
TTG Leu	TCT Ser	TTG Leu 575	AGA Arg	AAG Lys	AGC Ser	ATG Met	TCG Ser 580	AAA Lys	TAT Tyr	GAA Glu	TCA Ser	GAC Asp 585	AAC Asn	ATA Ile	AAG Lys	1957
TTA Leu 590	GAT Asp	GTC Val	CTT Leu	GGA Gly	TGG Trp	AGC Ser 595	AAA Lys	TAT Tyr	CAG Gln	CCT Pro	TGT Cys 600	TAT Tyr	CTT Leu	AAT Asn	CGT Arg	2005
CAA Gln 605	CTG Leu	ATT Ile	ACG Thr	CTC Leu	TTG Leu 610	TCT Ser	ACA Thr	CTT Leu	GGA Gly 615	GTG Val	AAA Lys	GAT Asp	GAA Glu	GTT Val	CTC Leu 620	2053
GAA Glu	CAG Gln	AAG Lys	CAA Gln	AAG Lys 625	GAA Glu	GCT Ala	GTA Val	GAT Asp	CAG Gln 630	CTT Leu	GAT Asp	GCT Ala	ATC Ile	TTG Leu 635	CAT His	2101
GAT Asp	TCT Ser	TTG Leu	AAG Lys 640	GCA Ala	CAG Gln	GAG Glu	GCT Ala 645	TTG Leu	GAA Glu	TTG Leu	ATG Met	TCT Ser	CCT Pro 650	GGA Gly	GAG Glu	2149
AAC Asn	ACT Thr	AAT Asn 655	ATT Ile	CTC Leu	AAG Lys	GCA Ala	ATG Met 660	CTA Leu	AAC Asn	TGT Cys	GGT Gly	TAT Tyr 665	AAG Lys	CCT Pro	GAT Asp	2197
GCT Ala	GAG Glu 670	CCC Pro	TTT Phe	CTT Leu	TCA Ser	ATG Met 675	ATG Met	TTG Leu	CAA Gln	ACC Thr 680	TTC Phe	CGC Arg	GCA Ala	TCC Ser	AAG Lys	2245

TTG CTC GAT TTG CGG ACT AGA TCA AGA ATA TTT ATT CCA AAT GGA AGA	2293
Leu Leu Asp Leu Arg Thr Arg Ser Arg Ile Phe Ile Pro Asn Gly Arg	
685 690 695 700	
ACA ATG ATG GGA TGT TTG GAT GAA TCC AGA ACC TTG GAA TAT GGT CAG	2341
Thr Met Met Gly Cys Leu Asp Glu Ser Arg Thr Leu Glu Tyr Gly Gln	
705 710 715	
GTG TTT GTT CAG TTT ACT GGT GCT GGA CAT GGA GAG TTT TCT GAC GAT	2389
Val Phe Val Gln Phe Thr Gly Ala Gly His Gly Glu Phe Ser Asp Asp	
720 725 730	
TTA CAT CCA TTT AAT AAC AGC AGA TCC ACC AAC AGT AAT TTC ATT CTG	2437
Leu His Pro Phe Asn Asn Ser Arg Ser Thr Asn Ser Asn Phe Ile Leu	
735 740 745	
AAG GGA AAT GTG GTT GTT GCA AAA AAT CCA TGC TTG CAT CCT GGT GAT	2485
Lys Gly Asn Val Val Val Ala Lys Asn Pro Cys Leu His Pro Gly Asp	
750 755 760	
ATT CGT GTT TTA AAG GCT GTA AAT GTT CGA GCG CTG CAC CAC ATG GTA	2533
Ile Arg Val Leu Lys Ala Val Asn Val Arg Ala Leu His His Met Val	
765 770 775 780	
GAT TGT GTT GTA TTC CCT CAG AAA GGA AAA AGA CCT CAT CCG AAT GAA	2581
Asp Cys Val Val Phe Pro Gln Lys Gly Lys Arg Pro His Pro Asn Glu	
785 790 795	
TGT TCT GGG AGT GAT TTG GAT GGG GAT ATC TAC TTT GTT TGC TGG GAT	2629
Cys Ser Gly Ser Asp Leu Asp Gly Asp Ile Tyr Phe Val Cys Trp Asp	
800 805 810	
CAA GAC ATG ATC CCG CCA AGG CAA GTC CAG CCG ATG GAA TAT CCT CCA	2677
Gln Asp Met Ile Pro Pro Arg Gln Val Gln Pro Met Glu Tyr Pro Pro	
815 820 825	
GCA CCC AGC ATA CAG TTG GAC CAT GAT GTC ACA ATT GAG GAA GTT GAA	2725
Ala Pro Ser Ile Gln Leu Asp His Asp Val Thr Ile Glu Glu Val Glu	
830 835 840	
GAG TAC TTC ACC AAC TAT ATT GTG AAT GAC AGT TTG GGA ATC ATA GCA	2773
Glu Tyr Phe Thr Asn Tyr Ile Val Asn Asp Ser Leu Gly Ile Ile Ala	
845 850 855 860	
AAT GCC CAT GTC GTA TTT GCA GAC AGA GAA CCT GAT ATG GCC ATG AGT	2821
Asn Ala His Val Val Phe Ala Asp Arg Glu Pro Asp Met Ala Met Ser	
865 870 875	
GAT CCA TGC AAA AAA CTT GCT GAG CTC TTT TCA ATT GCA GTG GAC TTT	2869
Asp Pro Cys Lys Lys Leu Ala Glu Leu Phe Ser Ile Ala Val Asp Phe	
880 885 890	
CCA AAG ACT GGT GTT CCC GCT GAA ATA CCA TCT CAG TTG CGC CCT AAA	2917
Pro Lys Thr Gly Val Pro Ala Glu Ile Pro Ser Gln Leu Arg Pro Lys	
895 900 905	
GAA TAC CCA GAC TTC ATG GAT AAG CCG GAC AAG ACC AGC TAT ATC TCA	2965
Glu Tyr Pro Asp Phe Met Asp Lys Pro Asp Lys Thr Ser Tyr Ile Ser	
910 915 920	

GAA AGA GTT ATT GGA AAG CTT TTC AGG AAA GTG AAG GAC AAA GCA CCT	3013
Glu Arg Val Ile Gly Lys Leu Phe Arg Lys Val Lys Asp Lys Ala Pro	
925 930 935 940	
CAG GCT AGC TCT ATC GCG ACC TTC ACA AGA GAT GTT GCA AGG AGA TCA	3061
Gln Ala Ser Ser Ile Ala Thr Phe Thr Arg Asp Val Ala Arg Arg Ser	
945 950 955	
TAT GAT GCT GAT ATG GAA GTT GAT GGA TTT GAA GAT TAC ATT GAC GAA	3109
Tyr Asp Ala Asp Met Glu Val Asp Gly Phe Glu Asp Tyr Ile Asp Glu	
960 965 970	
GCT TTT GAC TAC AAA ACT GAA TAT GAC AAC AAG CTG GGT AAT TTA ATG	3157
Ala Phe Asp Tyr Lys Thr Glu Tyr Asp Asn Lys Leu Gly Asn Leu Met	
975 980 985	
GAC TAC TAT GGC ATA AAA ACA GAG GCT GAA ATA CTT AGT GGT GGC ATT	3205
Asp Tyr Tyr Gly Ile Lys Thr Glu Ala Glu Ile Leu Ser Gly Gly Ile	
990 995 1000	
ATG AAG GCA TCA AAA ACT TTT GAC CGC AGA AAA GAT GCT GAG GCC ATT	3253
Met Lys Ala Ser Lys Thr Phe Asp Arg Arg Lys Asp Ala Glu Ala Ile	
1005 1010 1015 1020	
AGT GTT GCT GTG AGG GCC TTG AGG AAG GAG GCA AGA GCC TGG TTC AAG	3301
Ser Val Ala Val Arg Ala Leu Arg Lys Glu Ala Arg Ala Trp Phe Lys	
1025 1030 1035	
AGG CGT AAT GAT ATA GAT GAC ATG TTA CCA AAG GCT TCG GCT TGG TAC	3349
Arg Arg Asn Asp Ile Asp Asp Met Leu Pro Lys Ala Ser Ala Trp Tyr	
1040 1045 1050	
CAC GTT ACA TAT CAT CCT ACA TAT TGG GGT TGC TAC AAT CAG GGG TTG	3397
His Val Thr Tyr His Pro Thr Tyr Trp Gly Cys Tyr Asn Gln Gly Leu	
1055 1060 1065	
AAA AGA GCT CAT TTC ATT AGC TTT CCC TGG TGT GTT TAT GAC CAG CTA	3445
Lys Arg Ala His Phe Ile Ser Phe Pro Trp Cys Val Tyr Asp Gln Leu	
1070 1075 1080	
ATC CAG ATT AAG AAG GAC AAA GCA CGT AAC AGG CCA GTT CTC AAC TTG	3493
Ile Gln Ile Lys Lys Asp Lys Ala Arg Asn Arg Pro Val Leu Asn Leu	
1085 1090 1095 1100	
TCA TCT CTC AGG GCT CAA CTG AGT CAC AGA TTA GTG TTG AAA	3535
Ser Ser Leu Arg Ala Gln Leu Ser His Arg Leu Val Leu Lys	
1105 1110	
TGAGATTCCA GTCGAGCGTT AAGCTGATAT ATATATAATG TAATAGGGTG TGATCATAAG	3595
AAAACTGTTA TGCATTGTTG ACTACCTTTT GTCTTTTAAAA CTGCATGAAG CTGCAACATA	3655
TATGCAGTAC TCTAAGAAAC AGATGTACAG CTAAGTACTA ATATGTATGT GATTTGAGTT	3715
TCATCTTTCT TCTAAA	3731

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1114 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Gly Lys Thr Ile Gln Val Phe Gly Phe Pro Tyr Leu Leu Ser Ala
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Glu Val Val Lys Ser Phe Leu Glu Lys Tyr Thr Gly Tyr Gly Thr Val
          20           25           30
Cys Ala Leu Glu Val Lys Gln Ser Lys Gly Gly Ser Arg Ala Phe Ala
          35           40           45
Lys Val Gln Phe Ala Asp Asn Ile Ser Ala Asp Lys Ile Ile Thr Leu
          50           55           60
Ala Asn Asn Arg Leu Tyr Phe Gly Ser Ser Tyr Leu Lys Ala Trp Glu
          65           70           75           80
Met Lys Thr Asp Ile Val Gln Leu Arg Ala Tyr Val Asp Gln Met Asp
          85           90           95
Gly Ile Thr Leu Asn Phe Gly Cys Gln Ile Ser Asp Asp Lys Phe Ala
          100          105          110
Val Leu Gly Ser Thr Glu Val Ser Ile Gln Phe Gly Ile Gly Leu Lys
          115          120          125
Lys Phe Phe Phe Phe Leu Ser Ser Gly Ser Ala Asp Tyr Lys Leu Gln
          130          135          140
Leu Ser Tyr Glu Asn Ile Trp Gln Val Val Leu His Arg Pro Tyr Gly
          145          150          155          160
Gln Asn Ala Gln Phe Leu Leu Ile Gln Leu Phe Gly Ala Pro Arg Ile
          165          170          175
Tyr Lys Arg Leu Glu Asn Ser Cys Tyr Ser Phe Phe Lys Glu Thr Pro
          180          185          190
Asp Asp Gln Trp Val Arg Thr Thr Asp Phe Pro Pro Ser Trp Ile Gly
          195          200          205
Leu Ser Ser Ser Leu Cys Leu Gln Phe Arg Arg Gly Val Arg Leu Pro
          210          215          220
Asn Phe Glu Glu Ser Phe Phe His Tyr Ala Glu Arg Glu Asn Asn Ile
          225          230          235          240
Thr Leu Gln Thr Gly Phe Thr Phe Phe Val Ser Gln Lys Ser Ala Leu
          245          250          255
Val Pro Asn Val Gln Pro Pro Glu Gly Ile Ser Ile Pro Tyr Lys Ile
          260          265          270
Leu Phe Lys Ile Ser Ser Leu Val Gln His Gly Cys Ile Pro Gly Pro
          275          280          285

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Ala	Leu	Asn	Val	Tyr	Phe	Phe	Arg	Leu	Val	Asp	Pro	Arg	Arg	Arg	Asn	
290							295				300					
Val	Ala	Cys	Ile	Glu	His	Ala	Leu	Glu	Lys	Leu	Tyr	Tyr	Ile	Lys	Glu	
305					310					315					320	
Cys	Cys	Tyr	Asp	Pro	Val	Arg	Trp	Leu	Thr	Glu	Gln	Tyr	Asp	Gly	Tyr	
				325					330					335		
Leu	Lys	Gly	Arg	Gln	Pro	Pro	Lys	Ser	Pro	Ser	Ile	Thr	Leu	Asp	Asp	
			340					345					350			
Gly	Leu	Val	Tyr	Val	Arg	Arg	Val	Leu	Val	Thr	Pro	Cys	Lys	Val	Tyr	
		355					360					365				
Phe	Cys	Gly	Pro	Glu	Val	Asn	Val	Ser	Asn	Arg	Val	Leu	Arg	Asn	Tyr	
	370					375					380					
Ser	Glu	Asp	Ile	Asp	Asn	Phe	Leu	Arg	Val	Ser	Phe	Val	Asp	Glu	Glu	
385					390					395					400	
Trp	Glu	Lys	Leu	Tyr	Ser	Thr	Asp	Leu	Leu	Pro	Lys	Ala	Ser	Thr	Gly	
				405					410					415		
Ser	Gly	Val	Arg	Thr	Asn	Ile	Tyr	Glu	Arg	Ile	Leu	Ser	Thr	Leu	Arg	
			420					425					430			
Lys	Gly	Phe	Val	Ile	Gly	Asp	Lys	Lys	Phe	Glu	Phe	Leu	Ala	Phe	Ser	
		435					440					445				
Ser	Ser	Gln	Leu	Arg	Asp	Asn	Ser	Val	Trp	Met	Phe	Ala	Ser	Arg	Pro	
	450					455					460					
Gly	Leu	Thr	Ala	Asn	Asp	Ile	Arg	Ala	Trp	Met	Gly	Asp	Phe	Ser	Gln	
465					470					475					480	
Ile	Lys	Asn	Val	Ala	Lys	Tyr	Ala	Ala	Arg	Leu	Gly	Gln	Ser	Phe	Gly	
				485					490					495		
Ser	Ser	Arg	Glu	Thr	Leu	Ser	Val	Leu	Arg	His	Glu	Ile	Glu	Val	Ile	
			500					505					510			
Pro	Asp	Val	Lys	Val	His	Gly	Thr	Ser	Tyr	Val	Phe	Ser	Asp	Gly	Ile	
		515					520					525				
Gly	Lys	Ile	Ser	Gly	Asp	Phe	Ala	His	Arg	Val	Ala	Ser	Lys	Cys	Gly	
	530					535					540					
Leu	Gln	Tyr	Thr	Pro	Ser	Ala	Phe	Gln	Ile	Arg	Tyr	Gly	Gly	Tyr	Lys	
545					550					555					560	
Gly	Val	Val	Gly	Val	Asp	Pro	Asp	Ser	Ser	Met	Lys	Leu	Ser	Leu	Arg	
				565					570					575		
Lys	Ser	Met	Ser	Lys	Tyr	Glu	Ser	Asp	Asn	Ile	Lys	Leu	Asp	Val	Leu	
			580					585					590			
Gly	Trp	Ser	Lys	Tyr	Gln	Pro	Cys	Tyr	Leu	Asn	Arg	Gln	Leu	Ile	Thr	
		595					600					605				

Leu Leu Ser Thr Leu Gly Val Lys Asp Glu Val Leu Glu Gln Lys Gln
 610 615 620
 Lys Glu Ala Val Asp Gln Leu Asp Ala Ile Leu His Asp Ser Leu Lys
 625 630 635 640
 Ala Gln Glu Ala Leu Glu Leu Met Ser Pro Gly Glu Asn Thr Asn Ile
 645 650 655
 Leu Lys Ala Met Leu Asn Cys Gly Tyr Lys Pro Asp Ala Glu Pro Phe
 660 665 670
 Leu Ser Met Met Leu Gln Thr Phe Arg Ala Ser Lys Leu Leu Asp Leu
 675 680 685
 Arg Thr Arg Ser Arg Ile Phe Ile Pro Asn Gly Arg Thr Met Met Gly
 690 695 700
 Cys Leu Asp Glu Ser Arg Thr Leu Glu Tyr Gly Gln Val Phe Val Gln
 705 710 715 720
 Phe Thr Gly Ala Gly His Gly Glu Phe Ser Asp Asp Leu His Pro Phe
 725 730 735
 Asn Asn Ser Arg Ser Thr Asn Ser Asn Phe Ile Leu Lys Gly Asn Val
 740 745 750
 Val Val Ala Lys Asn Pro Cys Leu His Pro Gly Asp Ile Arg Val Leu
 755 760 765
 Lys Ala Val Asn Val Arg Ala Leu His His Met Val Asp Cys Val Val
 770 775 780
 Phe Pro Gln Lys Gly Lys Arg Pro His Pro Asn Glu Cys Ser Gly Ser
 785 790 795 800
 Asp Leu Asp Gly Asp Ile Tyr Phe Val Cys Trp Asp Gln Asp Met Ile
 805 810 815
 Pro Pro Arg Gln Val Gln Pro Met Glu Tyr Pro Pro Ala Pro Ser Ile
 820 825 830
 Gln Leu Asp His Asp Val Thr Ile Glu Glu Val Glu Glu Tyr Phe Thr
 835 840 845
 Asn Tyr Ile Val Asn Asp Ser Leu Gly Ile Ile Ala Asn Ala His Val
 850 855 860
 Val Phe Ala Asp Arg Glu Pro Asp Met Ala Met Ser Asp Pro Cys Lys
 865 870 875 880
 Lys Leu Ala Glu Leu Phe Ser Ile Ala Val Asp Phe Pro Lys Thr Gly
 885 890 895
 Val Pro Ala Glu Ile Pro Ser Gln Leu Arg Pro Lys Glu Tyr Pro Asp
 900 905 910
 Phe Met Asp Lys Pro Asp Lys Thr Ser Tyr Ile Ser Glu Arg Val Ile
 915 920 925

Gly Lys Leu Phe Arg Lys Val Lys Asp Lys Ala Pro Gln Ala Ser Ser
 930 935 940
 Ile Ala Thr Phe Thr Arg Asp Val Ala Arg Arg Ser Tyr Asp Ala Asp
 945 950 955 960
 Met Glu Val Asp Gly Phe Glu Asp Tyr Ile Asp Glu Ala Phe Asp Tyr
 965 970 975
 Lys Thr Glu Tyr Asp Asn Lys Leu Gly Asn Leu Met Asp Tyr Tyr Gly
 980 985 990
 Ile Lys Thr Glu Ala Glu Ile Leu Ser Gly Gly Ile Met Lys Ala Ser
 995 1000 1005
 Lys Thr Phe Asp Arg Arg Lys Asp Ala Glu Ala Ile Ser Val Ala Val
 1010 1015 1020
 Arg Ala Leu Arg Lys Glu Ala Arg Ala Trp Phe Lys Arg Arg Asn Asp
 1025 1030 1035 1040
 Ile Asp Asp Met Leu Pro Lys Ala Ser Ala Trp Tyr His Val Thr Tyr
 1045 1050 1055
 His Pro Thr Tyr Trp Gly Cys Tyr Asn Gln Gly Leu Lys Arg Ala His
 1060 1065 1070
 Phe Ile Ser Phe Pro Trp Cys Val Tyr Asp Gln Leu Ile Gln Ile Lys
 1075 1080 1085
 Lys Asp Lys Ala Arg Asn Arg Pro Val Leu Asn Leu Ser Ser Leu Arg
 1090 1095 1100
 Ala Gln Leu Ser His Arg Leu Val Leu Lys
 1105 1110

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Arg Thr Met Met Gly Cys Leu Asp Glu Ser Arg Thr Leu Glu Tyr Gly
 1 5 10 15
 Gln Val Phe Val Gln Phe Thr Gly Ala Gly His Gly Glu Phe Ser Asp
 20 25 30
 Asp Leu His Pro Phe Asn Asn Ser Arg Ser Thr Asn Ser Asn Phe Ile
 35 40 45
 Leu Lys Gly Asn Val Val Val Ala Lys Asn Pro Cys Leu His Pro Gly
 50 55 60

(2) INFORMATION FOR SEQ ID NO:4:

(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "primer"

CATAACGAAT CTGGAAAGCA GATGG

(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATGAATCCG GATCAACACC CACAC

25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGTGCTGGA GGATATTCCA TCGGC

25

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTTCACCAGG GATCCACTCA TCACTCCCCT CAAG

34

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCATAACTTC AGGGGGGATC CAGTTGGTGT TAGC

34

(2) INFORMATION FOR SEQ ID NO:9:

- ```
(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"
```

GCAGCTTCAT GCAGATCTAA AGACAAAAGG TAGTC

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Asn Arg Val Leu Arg Asn Tyr Ser Glu Asp Ile Asp Asn  
1 5 10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Ser Lys Thr Phe Asp Arg Arg Lys Asp Ala Glu Ala Ile  
1 5 10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gln | Tyr | Asp | Gly | Tyr | Leu | Lys | Gly | Arg | Gln | Pro | Pro | Lys | Ser | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Ser

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Pro | Gln | Lys | Gly | Lys | Arg | Pro | His | Asn | Glu | Cys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |

12345678910111213